# UNITED STATES PATENT AND TRADEMARK OFFICE

| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO. |
|---|---|---|---|---|
| 09/380,447 | 09/01/1999 | Sachdev S. Sidhu | 11669.141USWO | 2633 |

23552        7590        08/30/2007
MERCHANT & GOULD PC
P.O. BOX 2903
MINNEAPOLIS, MN 55402-0903

| EXAMINER |
|---|
| STEELE, AMBER D |

| ART UNIT | PAPER NUMBER |
|---|---|
| 1639 | |

| MAIL DATE | DELIVERY MODE |
|---|---|
| 08/30/2007 | PAPER |

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

PTOL-90A  (Rev. 04/07)

| APPLICATION NO. 09380447 | FILING DATE 9/1/1999 | FIRST NAMED INVENTOR SIDHU ET AL. | ATTORNEY DOCKET NO. 11669.141USWO |
|---|---|---|---|

MERCHANT & GOULD PC
P.O. BOX 2903
MINNEAPOLIS, MN 55402-0903

| EXAMINER |
|---|
| Amber D.. Steele |

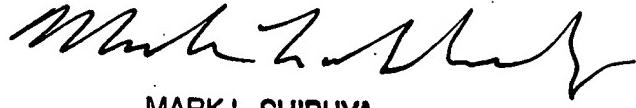| ART UNIT | PAPER |
|---|---|
| 1639 | 20070821 |

DATE MAILED:

**Please find below and/or attached an Office communication concerning this application or proceeding.**

Commissioner for Patents

1)The present application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821 (a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825. The sequence listing has various errors as indicated in the attached Raw Sequence Listing and error report.

2)Applicant is given ONE MONTH from the date of this letter within which to comply with the Sequence Rules, 37 CFR 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In NO case may an applicant extend the period for response beyond the six month statutory period. Applicant is requested to return a copy of the attached Notice to Comply with the response.

3)Any inquiry concerning this communication or earlier communications from the examiner should be directed to Amber D. Steele whose telephone number is 571-272-5538. The examiner can normally be reached Monday through Friday 9:00AM-5:00PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Doug Schultz can be reached at 571-272-0763. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300. Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

ADS
August 21, 2007

MARK L. SHIBUYA
PRIMARY EXAMINER

PTO-90C (Rev.04-03)

| **Notice to Comply** | Application No. 09/380,447 | Applicant(s) S IDHU ET AL. |
|---|---|---|
| | Examiner Steele, A. D. | Art Unit 1639 | |

## NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set in the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☒ 7. Other: see attached PTO-90C.

### Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", **as well as an amendment specifically directing its entry into the application.**

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (571) 272-2510
For CRF Submission Help, call (571) 272-2501/2583.
PatentIn Software Program Support
    Technical Assistance......................................703-287-0200
    To Purchase PatentIn Software.......................703-306-2600

### PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

```
==============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: Mon Jul 30 14:06:26 EDT 2007
==============================================================
```

```
********************************************************
Reviewer Comments:
<150> US 60/134,870
<151> 1999 05 19

<150> US 60/133,296
<151> 1999 05 10

<150> US 60/103,514
<151> 1998 10 08

<150> US 60/094,291
<151> 1998 07 27

<150> PCT/USUS99/16596
<151> 1999 07 22
```

The above non-ASCII characters ("squares") between dates appear
throughout the submitted sequence listing file; they also appear in
<222> responses which indicate locations within the sequence. Please
replace them with hyphens.

```
<400>   293
His His His His
   1
```

69

Please remove the above "69" appearing at the end of the submitted file.

Application No:    09380447          Version No:    3.0

Input Set:

Output Set:

|  |  |
|---|---|
| Started: | 2007-07-19 18:29:54.051 |
| Finished: | 2007-07-19 18:31:26.799 |
| Elapsed: | 0 hr(s) 1 min(s) 32 sec(s) 748 ms |
| Total Warnings: | 284 |
| Total Errors: | 366 |
| No. of SeqIDs Defined: | 292 |
| Actual SeqID Count: | 293 |

| Error code | Error Description |
|---|---|
| E 287 | Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <141> |
| E 287 | Invalid WIPO ST.2 date format; Use (YYYY-MM-DD)in <151> |
| E 287 | Invalid WIPO ST.2 date format; Use (YYYY-MM-DD)in <151> |
| E 287 | Invalid WIPO ST.2 date format; Use (YYYY-MM-DD)in <151> |
| E 287 | Invalid WIPO ST.2 date format; Use (YYYY-MM-DD)in <151> |
| E 287 | Invalid WIPO ST.2 date format; Use (YYYY-MM-DD)in <151> |
| W 213 | Artificial or Unknown found in <213>  in SEQ ID (1) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (12) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (13) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (14) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (15) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (16) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (17) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (18) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (19) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (20) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (21) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (22) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (23) |
| E 341 | 'Xaa' position not defined   SEQID (1)   POS (24) |

Input Set:

Output Set:

|                        |                                    |
|------------------------|------------------------------------|
| Started:               | 2007-07-19 18:29:54.051            |
| Finished:              | 2007-07-19 18:31:26.799            |
| Elapsed:               | 0 hr(s) 1 min(s) 32 sec(s) 748 ms  |
| Total Warnings:        | 284                                |
| Total Errors:          | 366                                |
| No. of SeqIDs Defined: | 292                                |
| Actual SeqID Count:    | 293                                |

| Error code | | Error Description |
|------|------|-------------------------------------------------|
| E | 341 | 'Xaa' position not defined   SEQID (1)  POS (25) |
| E | 341 | 'Xaa' position not defined   SEQID (1)  POS (26) |
| E | 341 | 'Xaa' position not defined   SEQID (1)  POS (27) |
| E | 341 | 'Xaa' position not defined   SEQID (1)  POS (28) |
| E | 341 | 'Xaa' position not defined   SEQID (1)  POS (29) |
| E | 341 | 'Xaa' position not defined   SEQID (1)  POS (30) |
| E | 257 | Invalid sequence data feature in <221>  in SEQ ID (2) |
| E | 257 | Invalid sequence data feature in <221>  in SEQ ID (3) |
| E | 257 | Invalid sequence data feature in <221>  in SEQ ID (4) |
| E | 257 | Invalid sequence data feature in <221>  in SEQ ID (5) |
| E | 257 | Invalid sequence data feature in <221>  in SEQ ID (6) |
| E | 257 | Invalid sequence data feature in <221>  in SEQ ID (7) |
| E | 257 | Invalid sequence data feature in <221>  in SEQ ID (8) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (9) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (10) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (11) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (12) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (13) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (14) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (15) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (16) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (17) |

```
                Input Set:


                Output Set:



                      Started:    2007-07-19 18:29:54.051
                     Finished:    2007-07-19 18:31:26.799
                      Elapsed:    0 hr(s) 1 min(s) 32 sec(s) 748 ms
              Total Warnings:     284
                Total Errors:     366
       No. of SeqIDs Defined:     292
           Actual SeqID Count:    293
```

| Error code | Error Description |
|---|---|
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (18) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (19) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (20) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (21) |
| E  342 | 'n' position not defined  found at POS:  20 SEQID(21) |
| E  342 | 'n' position not defined  found at POS:  22 SEQID(21) |
| E  342 | 'n' position not defined  found at POS:  26 SEQID(21) |
| E  342 | 'n' position not defined  found at POS:  28 SEQID(21) |
| E  342 | 'n' position not defined  found at POS:  31 SEQID(21) |
| E  342 | 'n' position not defined  found at POS:  34 SEQID(21) |
| E  342 | 'n' position not defined  found at POS:  38 SEQID(21) |
| E  342 | 'n' position not defined  found at POS:  41 SEQID(21) |
| E  342 | 'n' position not defined  found at POS:  44 SEQID(21) |
| E  342 | 'n' position not defined  found at POS:  47 SEQID(21) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (22) |
| E  342 | 'n' position not defined  found at POS:  19 SEQID(22) |
| E  342 | 'n' position not defined  found at POS:  22 SEQID(22) |
| E  342 | 'n' position not defined  found at POS:  26 SEQID(22) |
| E  342 | 'n' position not defined  found at POS:  28 SEQID(22) |
| E  342 | 'n' position not defined  found at POS:  31 SEQID(22) |
| E  342 | 'n' position not defined  found at POS:  35 SEQID(22) |
| E  342 | 'n' position not defined  found at POS:  38 SEQID(22) |

Input Set:

Output Set:

|  |  |
|---|---|
| Started: | 2007-07-19 18:29:54.051 |
| Finished: | 2007-07-19 18:31:26.799 |
| Elapsed: | 0 hr(s) 1 min(s) 32 sec(s) 748 ms |
| Total Warnings: | 284 |
| Total Errors: | 366 |
| No. of SeqIDs Defined: | 292 |
| Actual SeqID Count: | 293 |

| Error code | | Error Description |
|---|---|---|
| E | 342 | 'n' position not defined  found at POS:  41 SEQID(22) |
| E | 342 | 'n' position not defined  found at POS:  44 SEQID(22) |
| E | 342 | 'n' position not defined  found at POS:  46 SEQID(22)<br>This error has occured more than 20 times, will not be displayed |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (23) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (24) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (25) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (26) |
| W | 213 | Artificial or Unknown found in <213>  in SEQ ID (27)<br>This error has occured more than 20 times, will not be displayed |
| E | 257 | Invalid sequence data feature in <221>  in SEQ ID (36) |
| E | 257 | Invalid sequence data feature in <221>  in SEQ ID (56) |
| E | 355 | Empty lines found between the amino acid numbering and the |
| E | 321 | No. of Bases conflict, this line has no nucleotides  SEQID (293) |
| E | 252 | Calc# of Seq. differs from actual; 292 seqIds defined; count=293 |

<110> Sidhu, Sachdev S.
      Weiss, Gregory A.
      Wells, James A.

<120> TRANSFORMATION EFFICIENCY IN PHAGE DISPLAY THROUGH MODIFICATION OF A
      COAT PROTEIN

<130> 11669.141USWO

<140>  09380447
<141>  1999-09-01

<150>   US 09/380,447
<151>   1999 09 01

<150> US 60/134,870
<151> 1999 05 19

<150> US 60/133,296
<151> 1999 05 10

<150> US 60/103,514
<151> 1998 10 08

<150> US 60/094,291
<151> 1998 07 27

<150> PCT/USUS99/16596
<151> 1999 07 22

<160> 292

<210> 1
<211> 50
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic coat protein

<220>
<221> unsure
<222> 12 30
<223> unknown amino acid

<400> 1
 Met Ser Lys Ser Thr Phe Lys Lys Phe Leu Lys Xaa Xaa Xaa Xaa
  1               5               10                  15


 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                  20                  25                  30


 Glu Thr Ala Ser Ala Gln Leu Ser Asn Phe Ala Ala Lys Ala Pro
                  35                  40                  45

Asp Asp Gly Glu Ala
                    50


<210> 2

<211> 50
<212> PRT
<213> M13 phage

<220>
<221> M13 phage
<222> 1 50
<223> coat protein VIII

<400> 2
  Ala Glu Gly Asp Asp Pro Ala Lys Ala Ala Phe Asn Ser Leu Gln
   1               5                  10                  15

  Ala Ser Ala Thr Glu Tyr Ile Gly Tyr Ala Trp Ala Met Val Val
                  20                  25                  30

  Val Ile Val Gly Ala Thr Ile Gly Ile Lys Leu Phe Lys Lys Phe
                  35                  40                  45

  Thr Ser Lys Ala Ser
                  50


<210> 3
<211> 50
<212> PRT
<213> f1 phage

<220>
<221> f1 phage
<222> 1 50
<223> coat protein VIII

<400> 3
  Ala Glu Gly Asp Asp Pro Ala Lys Ala Ala Phe Asp Ser Leu Gln
   1               5                  10                  15

  Ala Ser Ala Thr Glu Tyr Ile Gly Tyr Ala Trp Ala Met Val Val
                  20                  25                  30

  Val Ile Val Gly Ala Thr Ile Gly Ile Lys Leu Phe Lys Lys Phe
                  35                  40                  45

  Thr Ser Lys Ala Ser
                  50


<210> 4
<211> 50
<212> PRT
<213> fd phage

<220>
<221> fd phage

<222> 1 50
<223> coat protein VIII


<400> 4
Ala Glu Gly Asp Asp Pro Ala Lys Ala Ala Phe Asp Ser Leu Gln
1               5               10              15


Ala Ser Ala Thr Glu Tyr Ile Gly Tyr Ala Trp Ala Met Val Val
                20              25              30


Val Ile Val Gly Ala Thr Ile Gly Ile Lys Leu Phe Lys Lys Phe
                35              40              45


Thr Ser Lys Ala Ser
                50

<210> 5
<211> 50
<212> PRT
<213> Zj 2 phage


<220>
<221> Zj 2 phage
<222> 1 50
<223> coat protein VIII


<400> 5
Ala Glu Gly Asp Asp Pro Ala Lys Ala Ala Phe Asp Ser Leu Gln
1               5               10              15


Ala Ser Ala Thr Glu Tyr Ile Gly Tyr Ala Trp Ala Met Val Val
                20              25              30


Val Ile Val Gly Ala Thr Ile Gly Ile Lys Leu Phe Lys Lys Phe
                35              40              45


Ala Ser Lys Ala Ser
                50


<210> 6
<211> 50
<212> PRT
<213> Ifl phage


<220>
<221> Ifl phage
<222> 1 50
<223> coat protein VIII


<400> 6
Asp Asp Ala Thr Ser Gln Ala Lys Ala Ala Phe Asp Ser Leu Thr
1               5               10              15


Ala Gln Ala Thr Glu Met Ser Gly Tyr Ala Trp Ala Leu Val Val
                20              25              30

```
Leu Val Val Gly Ala Thr Val Gly Ile Lys Leu Phe Lys Lys Phe
                35                    40                    45


Val Ser Arg Ala Ser
                50


<210> 7
<211> 50
<212> PRT
<213> I2 2 phage


<220>
<221> I2 2 phage
<222> 1 50
<223> coat protein VIII


<400> 7
Ser Thr Ala Thr Ser Tyr Ala Thr Glu Ala Met Asn Ser Leu Lys
  1               5                   10                  15


Thr Gln Ala Thr Asp Leu Ile Asp Gln Thr Trp Pro Val Val Thr
                20                    25                    30


Ser Val Ala Val Ala Gly Leu Ala Ile Arg Leu Phe Lys Lys Phe
                35                    40                    45


Ser Ser Lys Ala Val
                50


<210> 8
<211> 50
<212> PRT
<213> Ike phage


<220>
<221> Ike phage
<222> 1 50
<223> coat protein VIII


<400> 8
Asn Ala Ala Thr Asn Tyr Ala Thr Glu Ala Met Asp Ser Leu Lys
  1               5                   10                  15


Thr Gln Ala Ile Asp Leu Ile Ser Gln Thr Trp Pro Val Val Thr
                20                    25                    30


Thr Val Val Val Ala Gly Leu Val Ile Arg Leu Phe Lys Lys Phe
                35                    40                    45


Ser Ser Lys Ala Val
                50


<210> 9
<211> 30
<212> DNA
<213> Artificial sequence
```

<220>
<223> oligonucleotide primer

<400> 9
aaaagaattc ccgacaccat cgaatggtgc 30

<210> 10
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide primer

<400> 10
accagatgca taagccgagg cggaaaacat catcg 35

<210> 11
<211> 56
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide primer

<400> 11
ttttctagac aggcctccca ccagatgcat aagccgaggc ggaaaacatc 50

atcgtc 56

<210> 12
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide primer

<400> 12
gctatcggaa tgcatcgggc atcaccggca cctg 34

<210> 13
<211> 61
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide primer

<400> 13
gagtcatagt cgtcaggcgc ctcctccgga tcctccaccc accttggtga 50

aggtgtcgtg g 61

<210> 14

<211> 18
<212> DNA
<213> Artificial sequence

<220>

<223> oligonucleotide primer

<400> 14
 gggtatctag aggttgag 18

<210> 15
<211> 46
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide primer

<400> 15
 tggagctccc ggatcctcca ccgctctgga agccacagct gccctc 46

<210> 16
<211> 42
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 16
 ggatccggga gctccagctg atgaggtgac gatcccgcaa aa 42

<210> 17
<211> 42
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 17
 gatcccgcaa aagcggcctg atgatccctg caagcctcag cg 42

<210> 18
<211> 42
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 18
 caagcctcag cgaccgaatg atgaggttat gcgtgggcga tg 42

<210> 19
<211> 42

<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide


<400> 19
cgctgggcga tggttgtttg atgagtcggc gcaactatcg gt 42


<210> 20
<211> 42
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 20
gcaactatcg gtatcaagtg atgaaagaaa ttcacctcga aa 42


<210> 21
<211> 66
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<220>
<221> unsure
<222> 20, 22, 26, 28, 31, 34, 38, 41, 44, 47
<223> unknown base


<400> 21
ggatccggga gctccagcrn tnasrntnas nasnycrntr narntrnttt 50

taactccctg caagcc 66


<210> 22
<211> 66
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<220>
<221> unsure
<222> 19, 22, 26, 28, 31, 35, 38, 41, 44, 46
<223> unknown base


<400> 22
gatcccgcaa aagcggccnw tnasrntnyt nasrntrntr ntrntnasta 50

tatcggttat gcgtgg 66

<210> 23
<211> 70
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<220>
<221> unsure
<222> 19, 22, 25, 28, 31, 35, 38, 41, 44, 47
<223> unknown base

<400> 23
 caagcctcag cgaccgaanw cnwcnktnwc nyytnkgnyt nkgnwtnwtg 50

 tcattgtcgg cgcaactatc 70

<210> 24
<211> 66
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<220>
<221> unsure
<222> 19, 22, 25, 28, 31, 34, 37 38, 40 41, 43 44
<223> unknown base

<400> 24
 gcgtgggcga tggttgttnw tnwcnwtnkt nytnytnntn ntnntaagct 50

 gtttaagaaa ttcacc 66

<210> 25
<211> 72
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<220>
<221> unsure
<222> 19 20, 22 23, 31 32, 34 35, 37 38, 43 44, 46 47
<223> unknown base

<400> 25
 gcaactatcg gtatcaagnn gnnsaagaaa nnsnngnnga aanngnngtg 50

 ataaaccgat acaattaaag gc 72

<210> 26
<211> 66
<212> DNA

<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 26
gatcccgcaa aagcggccta tgaggctctt gaggatattg ctactaacta 50


tatcggttat gcgtgg 66

<210> 27
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 27
ccgacaccct ccaatgctga ggaaacacaa cagaaa 36

<210> 28
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 28
ttcaggaagg acatggctaa ggtcgagaca ttcctg 36

<210> 29
<211> 75
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 29
aactacgggc tgctcgcttg cttcaggaag gacatggaca aggtcgagac 50


attcctggct atcgtgcagt gccgc 75

<210> 30
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 30
ttcaggaagg acatggacgc tgtcgagaca ttcctggcta tcgtccagtg 50

ccgctct 57

<210> 31
<211> 42
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 31
ggtggaggat ccgggagctg atgagccgag ggtgacgatc cc 42

<210> 32
<211> 46
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 32
caccaaggtg gtctagagct aataataagc cgagggtgac gatccc 46

<210> 33
<211> 50
<212> PRT
<213> Artificial sequence

<220>
<223> P12 1 variant

<400> 33
Met Ser Lys Ser Thr Phe Lys Lys Phe Leu Lys Val Phe Val Phe
1               5                   10                  15

Ser Val Asp Val Asp Asn Asn Trp Ile Trp Ala Val Gly Ile Ile
                20                  25                  30

Tyr Met Leu Leu Val Glu Ala Ser Pro Trp Ala Ala Lys Ala Pro
                35                  40                  45

Asp Asp Gly Glu Ala
                50

<210> 34
<211> 93
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide linker library

<400> 34
gagggcagct gtggcttcgg tggcggtvvc vvcvvcvvcv vcvvcvvcvv 50

cvvcvvcvvc vvcvvcvvcg gcggtgccga gggtgacgat ccc 93

<210> 35
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide linker library

<400> 35

  caccaaggtg gtctagagvv cvvcvvcvvc vvcgccgagg gtgacgatcc 50

  c 51

<210> 36
<211> 67
<212> DNA
<213> Artifical sequence

<220>
<221> Artificial sequence
<222> 1 67
<223> oligonucleotide linker library

<400> 36
  caccaaggtg gtctagagcv vcvvcvvcvv cvvcvvcvvc vvcvvcvvcg 50

  ccgagggtga cgatccc 67

<210> 37
<211> 82
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide linker library

<400> 37
  caccaaggtg gtctagagcv vcvvcvvcvv cvvcvvcvvc vvcvvcvvcv 50

  vcvvcvvcvv cvvcgccgag ggtgacgatc cc 82

<210> 38
<211> 97
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide linker library

<400> 38
  caccaaggtg gtctagagcv vcvvcvvcvv cvvcvvcvvc vvcvvcvvcv 50

  vcvvcvvcvv cvvcvvcvvc vvcvvcvvcg ccgagggtga cgatccc 97

<210> 39

<211> 112
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide linker library

<400> 39
caccaaggtg gtctagagcv vcvvcvvcvv cvvcvvcvvc vvcvvcvvcv 50

vcvvcvvcvv cvvcvvcvvc vvcvvcvvcv vcvvcvvcvv cvvcgccgag 100

ggtgacgatc cc 112

<210> 40
<211> 66
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 40
aagttcgcta gagatgctta tgaggctctt gaggatattg ctactaacta 50

tatcggttat gcgtgg 66

<210> 41
<211> 66
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 41
gaggatattg ctactaacct tttctttctc cttgggactg tgcatcttgt 50

cattgtcggc gcaact 66

<210> 42
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 42
gcaaaagcgg cctataacgc tcttgaggat att 33

<210> 43
<211> 33
<212> DNA
<213> Artificial sequence

<220>

&lt;400&gt; 43
tatgaggctc ttgaggccat tgctactaac tat 33

&lt;210&gt; 44
&lt;211&gt; 33
&lt;212&gt; DNA
&lt;213&gt; Artificial sequence

&lt;220&gt;
&lt;223&gt; mutagenic oligonucleotide

&lt;400&gt; 44
gaggctcttg aggattcagc tactaactat atc 33

&lt;210&gt; 45
&lt;211&gt; 66
&lt;212&gt; DNA
&lt;213&gt; Artificial sequence

&lt;220&gt;
&lt;223&gt; mutagenic oligonucleotide

&lt;400&gt; 45
gatcccgcaa aagcggccta tgaggctctt gaggatattg ctactaacta 50

tatcggttat gcgtgg 66

&lt;210&gt; 46
&lt;211&gt; 66
&lt;212&gt; DNA
&lt;213&gt; Artificial sequence

&lt;220&gt;
&lt;223&gt; mutagenic oligonucleotide

&lt;400&gt; 46
gagggcagct gtggcttcca gagcggtgga ggatccggga gctccagcgc 50

cgagggtgac gatccc 66

&lt;210&gt; 47
&lt;211&gt; 60
&lt;212&gt; DNA
&lt;213&gt; Artificial sequence

&lt;220&gt;
&lt;223&gt; mutagenic oligonucleotide

&lt;400&gt; 47
cccgcaaaag cggcctttaa cgctctgcaa gccattgcga ccgaatatat 50

cggttatgcg 60

&lt;210&gt; 48
&lt;211&gt; 66

<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 48
caagcctcag cgaccgaact tttctttctc cttgggactg tgcatcttgt 50

cattgtcggc gcaact 66

<210> 49
<211> 33

<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 49
tccgggagct ccagcgccaa gagtgagaag ttc 33

<210> 50
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 50
gggagctcca gcgatgagag tgagaagttc gct 33

<210> 51
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 51
agctccagcg ataagggtga gaagttcgct aga 33

<210> 52
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 52
tccagcgata agagtgacaa gttcgctaga gat 33

<210> 53

<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 53
agcgataaga gtgaggattt cgctagagat gct 33

<210> 54
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 54
gataagagtg agaagcccgc tagagatgct ttt 33

<210> 55
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 55
agtgagaagt cgctaaaga tgcttttaac tcc 33

<210> 56
<211> 33
<212> DNA
<213> Artifical sequence

<220>
<221> Artificial sequence
<222> 1 33
<223> mutagenic oligonucleotide

<400> 56
gagaagttcg ctagagcggc ttttaactcc ctg 33

<210> 57
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 57
cccgcaaaag cggcctttga ggctcttgag gat 33

<210> 58

<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 58
gcaaaagcgg cctataaacg ctcttgagga tatt 34

<210> 59
<211> 33
<212> DNA
<213> Artificial sequence


<220>
<223> mutagenic oligonucleotide

<400> 59
aaagcggcct atgagtccct tgaggatatt gct 33

<210> 60
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 60
gcctatgagg ctcttcaaga tattgctact aac 33

<210> 61
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 61
tatgaggctc ttgaggccat tgctactaac tat 33

<210> 62
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 62
gaggctcttg aggattcagc tactaactat atc 33

<210> 63
<211> 33

<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 63
 gaggatattg ctactgaata tatcggttat gcg 33


<210> 64
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 64
 gcctcagcga ccgaatattt ctttctcctt ggg 33


<210> 65
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 65
 tcagcgaccg aacttatctt tctccttggg act 33


<210> 66
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 66
 gcgaccgaac ttttcggtct ccttgggact gtg 33


<210> 67
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 67
 accgaacttt tcttttatct tgggactgtg cat 33


<210> 68
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 68
 gaacttttct ttctcgcggg gactgtgcat ctt 33

<210> 69
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 69
 cttttctttc tcctttggac tgtgcatctt gtc 33

<210> 70
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 70
 ttctttctcc ttggggcggt gcatcttgtc att 33

<210> 71
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 71
 tttctccttg ggactatgca tcttgtcatt gtc 33

<210> 72
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 72
 ctccttggga ctgtggttct tgtcattgtc ggc 33

<210> 73
<211> 33
<212> DNA
<213> Artificial sequence

<220>

<223> mutagenic oligonucleotide

<400> 73
cttgggactg tgcatgttgt cattgtcggc gca 33

<210> 74
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 74
gcaaaagcgg cctataactc ccttgaggat attgct 36

<210> 75
<211> 48

<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 75
gcaaaagcgg cctataacgc tcttgaggat tcagctacta actatatc 48

<210> 76
<211> 60
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 76
cccgcaaaag cggcctatga gtcccttgag gattcagcta ctaactatat 50

cggttatgcg 60

<210> 77
<211> 48
<212> DNA
<213> Artificial sequence

<220>
<223> mutagenic oligonucleotide

<400> 77
gcaaaagcgg cctataactc ccttgaggat tcagctacta actatatc 48

<210> 78
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> peptide linker

<40